

CRF Errors Corrected by the STIC Systems Branch.

Serial Number: 09/607,745

ENTERED

CRF Processing Date: 12/14/2003

Edited by: (initials)

Verified by: (initials)

1600
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12/14/2003
TECH CENTER 1600/2900

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☒ Other: Sequence 9 - aligned amino acid number

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

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1600

RAW SEQUENCE LISTING

DATE: 03/18/2003

PATENT APPLICATION: US/09/607,745

TIME: 18:41:22

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\03182003\I607745.raw

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3 <110> APPLICANT: Darrow, Andrew L
4   Qi, Jain-shen
5   Andrade-Gordon, Patricia
7 <120> TITLE OF INVENTION: DNA encoding human serine protease D-G
9 <130> FILE REFERENCE: ORT-1273
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/607,745
C--> 12 <141> CURRENT FILING DATE: 2000-06-30
14 <160> NUMBER OF SEQ ID NOS: 9
16 <170> SOFTWARE: PatentIn Ver. 2.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 2121
20 <212> TYPE: DNA
21 <213> ORGANISM: Homo sapiens
23 <400> SEQUENCE: 1
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25 atacacagag agaggcagca gcttgctcag cggacaagga tgctgggcgt gagggacca 120
26 ggccctgccct gcaactgggc ctcctccagc cagtgtctgac cagggaacttc tgacctgctg 180
27 gccagccagg acctgtgtgg ggaggccctc ctgctgcctt ggggtgacaa tctcagctcc 240
28 aggctacagg gagaccggga ggatcacaga gccagcatgg atcctgacag tgatcaacct 300
29 ctgaacagcc tcgatgtcaa acccctgcgc aaaccccgta tcccatgga gaccttcaga 360
30 aagggtgggga tccccatcat catagcacta ctgagcctgg cgagtatcat cattgtggtt 420
31 gtccctcatca aggtgattct ggataaatac tacttctctt gcgggcagcc tctccacttc 480
32 atcccgagga agcagctgtg tgacggagag ctggactgtc ccttggggga ggacgaggag 540
33 cactgtgtca agagcttccc cgaagggcct gcagtggcag tccgcctctc caaggaccga 600
34 tccacactgc aggtgtctga ctcgccaca gggaaactggt tctctgcctg ttctgacaac 660
35 ttcacagaag ctctcgtctg gacagcctgt aggcagatgg gctacagcag caaacccact 720
36 ttcagagctg tggagattgg ccagaccag gatctggatg ttgttgaaat cacagaaaac 780
37 agccaggagc ttgcgatgcg gaactcaagt gggccctgtc tctcaggctc cctggtctcc 840
38 ctgcaactgtc ttgcctgtgg gaagagcctg aagacccccc gtgtggtggg tggggaggag 900
39 gcctctgtgg attcttggcc ttggcaggtc agcatccagt acgacaaaca gcacgtctgt 960
40 ggaggaggca tcctggaccc ccaactgggtc ctacggcag ccaactgctt caggaaacat 1020
41 accgatgtgt tcaactggaa ggtgcgggca ggctcagaca aactgggcag cttcccctcc 1080
42 ctggctgtgg ccaagatcat catcattgaa ttcaacccca tgtaccccaa agacaatgac 1140
43 atgcacctca tgaagctgca gttcccactc accttctcag gcacagtcag gccactctgt 1200
44 ctgcccctct tctgatgagg gctcactcca gccacccac tctggatcat tggatggggc 1260
45 tttacgaagc agaattggag gaagatgtct gcataactgc tgcaggcgtc agtccaggtc 1320
46 attgacagca cacggtgcaa tgcagacgat gcgtacctgg gggaagtcac cgagaagatg 1380
47 atgtgtgcag gcatcccgga agggggtgtg gacacctgcc aggggtgacag tgggtggccc 1440
48 ctgatgtacc aatctgacca gtggcatgtg gtgggcctcg ttagctgggg ctatggctgc 1500
49 gggggcccgga gcaccccgag ggtatacacc aaggtctcag cctatctcaa ctggatctac 1560
50 aatgtctgga aggtgagct gtaatgtctg tgcccctttg cagtgtctgg agccgcttcc 1620
51 ttcctgcctt gccacctgg ggatcccca aagtcagaca cagagcaaga gtccccttgg 1680
52 gtacacccct ctgcccacag cctcagcatt tcttgagca gcaaagggcc tcaattccta 1740

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53 taagagaccc tcgcagccca gaggcgccc gaggaagtca gcagccctag ctgggccaca 1800
54 cttggtgctc ccagcatccc agggagagac acagcccact gaacaaggctc tcaggggtat 1860
55 tgctaagcca agaaggaact ttcccacact actgaatgga agcaggctgt cttgtaaaag 1920
56 cccagatcac tgtgggctgg agaggagaag gaaagggctc gcgccagccc tgtccgtctt 1980
57 caccatccc caagcctact agagcaagaa accagttgta atataaaatg cactgcctac 2040
58 tgttggtatg actaccgtta cctactgttg tcattgttat tacagctatg gccactatta 2100
59 ttaaagagct gtgtaacatc a                                     2121
62 <210> SEQ ID NO: 2
63 <211> LENGTH: 435
64 <212> TYPE: PRT
65 <213> ORGANISM: Homo sapiens
67 <400> SEQUENCE: 2
68 Met Asp Pro Asp Ser Asp Gln Pro Leu Asn Ser Leu Asp Val Lys Pro
69   1           5           10           15
71 Leu Arg Lys Pro Arg Ile Pro Met Glu Thr Phe Arg Lys Val Gly Ile
72           20           25           30
74 Pro Ile Ile Ile Ala Leu Leu Ser Leu Ala Ser Ile Ile Ile Val Val
75           35           40           45
77 Val Leu Ile Lys Val Ile Leu Asp Lys Tyr Tyr Phe Leu Cys Gly Gln
78           50           55           60
80 Pro Leu His Phe Ile Pro Arg Lys Gln Leu Cys Asp Gly Glu Leu Asp
81   65           70           75           80
83 Cys Pro Leu Gly Glu Asp Glu Glu His Cys Val Lys Ser Phe Pro Glu
84           85           90           95
86 Gly Pro Ala Val Ala Val Arg Leu Ser Lys Asp Arg Ser Thr Leu Gln
87           100          105          110
89 Val Leu Asp Ser Ala Thr Gly Asn Trp Phe Ser Ala Cys Phe Asp Asn
90           115          120          125
92 Phe Thr Glu Ala Leu Ala Glu Thr Ala Cys Arg Gln Met Gly Tyr Ser
93           130          135          140
95 Ser Lys Pro Thr Phe Arg Ala Val Glu Ile Gly Pro Asp Gln Asp Leu
96 145          150          155          160
98 Asp Val Val Glu Ile Thr Glu Asn Ser Gln Glu Leu Arg Met Arg Asn
99           165          170          175
101 Ser Ser Gly Pro Cys Leu Ser Gly Ser Leu Val Ser Leu His Cys Leu
102           180          185          190
104 Ala Cys Gly Lys Ser Leu Lys Thr Pro Arg Val Val Gly Gly Glu Glu
105           195          200          205
107 Ala Ser Val Asp Ser Trp Pro Trp Gln Val Ser Ile Gln Tyr Asp Lys
108           210          215          220
110 Gln His Val Cys Gly Gly Ser Ile Leu Asp Pro His Trp Val Leu Thr
111 225          230          235          240
113 Ala Ala His Cys Phe Arg Lys His Thr Asp Val Phe Asn Trp Lys Val
114           245          250          255
116 Arg Ala Gly Ser Asp Lys Leu Gly Ser Phe Pro Ser Leu Ala Val Ala
117           260          265          270
119 Lys Ile Ile Ile Ile Glu Phe Asn Pro Met Tyr Pro Lys Asp Asn Asp
120           275          280          285
122 Ile Ala Leu Met Lys Leu Gln Phe Pro Leu Thr Phe Ser Gly Thr Val

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123      290      295      300
125 Arg Pro Ile Cys Leu Pro Phe Phe Asp Glu Glu Leu Thr Pro Ala Thr
126 305      310      315      320
128 Pro Leu Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln Asn Gly Gly Lys
129-      325      330      335
131 Met Ser Asp Ile Leu Leu Gln Ala Ser Val Gln Val Ile Asp Ser Thr
132      340      345      350
134 Arg Cys Asn Ala Asp Asp Ala Tyr Gln Gly Glu Val Thr Glu Lys Met
135      355      360      365
137 Met Cys Ala Gly Ile Pro Glu Gly Gly Val Asp Thr Cys Gln Gly Asp
138      370      375      380
140 Ser Gly Gly Pro Leu Met Tyr Gln Ser Asp Gln Trp His Val Val Gly
141 385      390      395      400
143 Ile Val Ser Trp Gly Tyr Gly Cys Gly Gly Pro Ser Thr Pro Gly Val
144      405      410      415
146 Tyr Thr Lys Val Ser Ala Tyr Leu Asn Trp Ile Tyr Asn Val Trp Lys
147      420      425      430
149 Ala Glu Leu
150      435
153 <210> SEQ ID NO: 3
154 <211> LENGTH: 20
155 <212> TYPE: DNA
156 <213> ORGANISM: Artificial Sequence
158 <220> FEATURE:
159 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
160     oligonucleotide primer
162 <400> SEQUENCE: 3
163 acagcctcag cattttcttgg                      20
166 <210> SEQ ID NO: 4
167 <211> LENGTH: 20
168 <212> TYPE: DNA
169 <213> ORGANISM: Artificial Sequence
171 <220> FEATURE:
172 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
173     oligonucleotide primer
175 <400> SEQUENCE: 4
176 tcttgctcta gtaggcttgg                      20
179 <210> SEQ ID NO: 5
180 <211> LENGTH: 40
181 <212> TYPE: DNA
182 <213> ORGANISM: Artificial Sequence
184 <220> FEATURE:
185 <223> OTHER INFORMATION: Description of Artificial Sequence: Nested probe
187 <400> SEQUENCE: 5
188 ttggtgctcc cagcatccca gggagagaca cagcccactg          40
191 <210> SEQ ID NO: 6
192 <211> LENGTH: 30
193 <212> TYPE: DNA
194 <213> ORGANISM: Artificial Sequence

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196 <220> FEATURE:
197 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
198     oligonucleotide primer
200 <400> SEQUENCE: 6
201 atgctctaga tgtggattct tggccttgcc           30
204 <210> SEQ ID NO: 7
205 <211> LENGTH: 32
206 <212> TYPE: DNA
207 <213> ORGANISM: Artificial Sequence
209 <220> FEATURE:
210 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
211     oligonucleotide primer
213 <400> SEQUENCE: 7
214 gatgtctaga cagctcagcc ttccagacat tg           32
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218 <211> LENGTH: 1189
219 <212> TYPE: DNA
220 <213> ORGANISM: Artificial Sequence
222 <220> FEATURE:
223 <223> OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
225 <400> SEQUENCE: 8
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227 gtggtgtcaa atctactctt gtgccagggt gtggtctccg actacaagga cgacgacgac 120
228 gtggacgcgg ccgctcttgc tgcccccttt gatgatgatg acaagatcgt tgggggctat 180
229 gctctagatg tggattcttg gccttggcag gtcagcatcc agtacgacaa acagcacgtc 240
230 tgtggaggga gcatcctgga cccccactgg gtcctcacgg cagccactg cttcaggaaa 300
231 cataccgatg tgttcaactg gaagggtgcg gcaggctcag acaaactggg cagcttccca 360
232 tccctggctg tggccaagat catcatcatt gaattcaacc ccatgtaccc caaagacaat 420
233 gacatgcgcc tcatgaagct gcagttccca ctactttct caggcacagt caggcccatc 480
234 tgtctgccct tctttgatga ggagctcact ccagccaccc cactctggat cattggatgg 540
235 ggctttacga agcagaatgg agggaagatg tctgacatac tgctgcaggc gtcagtccag 600
236 gtcattgaca gcacacgggt caatgcagac gatgcgtacc tgggggaagt caccgagaag 660
237 atgatgtgtg caggcatccc ggaagggggt gtggacacct gccagggtga cagtgggtgg 720
238 cccctgatgt accaatctga ccagtggcat gtggtgggca tcgttagctg gggctatggc 780
239 tgcggggggc cgagcacccc aggggtatac accaaggtct cagcctatct caactggatc 840
240 tacaatgtct ggaaggetga gctgtctaga catcaccatc accatcacta gcggccgctt 900
241 cccttttagt aggggttaat ctctgagcag acatgataag atacattgat gagtttggac 960
242 aaaccacaac tagaatgcag tgaaaaaaat gctttatttg tgaaatttgt gatgctattg 1020
243 ctttatttgt aaccattata agctgcaata aacaagttag cttgtcgaga agtactagag 1080
244 gatcataatc agccatacca catttgtaga ggttttactt gctttaaaaa acctcccaca 1140
245 cctccccctg aacctgaaac ataaaatgaa tgcaattggt gttgttaac           1189
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249 <211> LENGTH: 292
250 <212> TYPE: PRT
251 <213> ORGANISM: Artificial Sequence
253 <220> FEATURE:
254 <223> OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
256 <400> SEQUENCE: 9
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258      1              5              10              15
260 Val Val Ser Asn Leu Leu Leu Cys Gln Gly Val Val Ser Asp Tyr Lys
261              20              25              30
263 Asp Asp Asp Asp Val Asp Ala Ala Leu Ala Ala Pro Phe Asp Asp
264              35              40              45
266 Asp Asp Lys Ile Val Gly Gly Tyr Ala Leu Asp Val Asp Ser Trp Pro
267              50              55              60
269 Trp Gln Val Ser Ile Gln Tyr Asp Lys Gln His Val Cys Gly Gly Ser
270      65              70              75              80
272 Ile Leu Asp Pro His Trp Val Leu Thr Ala Ala His Cys Phe Arg Lys
273              85              90              95
275 His Thr Asp Val Phe Asn Trp Lys Val Arg Ala Gly Ser Asp Lys Leu
276              100             105             110
278 Gly Ser Phe Pro Ser Leu Ala Val Ala Lys Ile Ile Ile Ile Glu Phe
279              115             120             125
281 Asn Pro Met Tyr Pro Lys Asp Asn Asp Ile Ala Leu Met Lys Leu Gln
282              130             135             140
284 Phe Pro Leu Thr Phe Ser Gly Thr Val Arg Pro Ile Cys Leu Pro Phe
285      145             150             155             160
287 Phe Asp Glu Glu Leu Thr Pro Ala Thr Pro Leu Trp Ile Ile Gly Trp
288              165             170             175
290 Gly Phe Thr Lys Gln Asn Gly Gly Lys Met Ser Asp Ile Leu Leu Gln
291              180             185             190
293 Ala Ser Val Gln Val Ile Asp Ser Thr Arg Cys Asn Ala Asp Asp Ala
294              195             200             205
296 Tyr Gln Gly Glu Val Thr Glu Lys Met Met Cys Ala Gly Ile Pro Glu
297              210             215             220
299 Gly Gly Val Asp Thr Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Tyr
300      225             230             235             240
302 Gln Ser Asp Gln Trp His Val Val Gly Ile Val Ser Trp Gly Tyr Gly
303              245             250             255
305 Cys Gly Gly Pro Ser Thr Pro Gly Val Tyr Thr Lys Val Ser Ala Tyr
306              260             265             270
308 Leu Asn Trp Ile Tyr Asn Val Trp Lys Ala Glu Leu Ser Arg His His
309              275             280             285
311 His His His His
312              290

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VERIFICATION SUMMARY

DATE: 03/18/2003

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Input Set : A:\PTO.AMC.txt

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L:11 M:270 C: Current Application Number differs, Replaced Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date